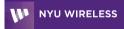
Seeded Database Matching Under Noisy Column Repetitions

Serhat Bakirtas, Elza Erkip

New York University





Information Theory Workshop 2022



2 Background





5 Conclusion

S. Bakirtas, E. Erkip



• Age of data collection.





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- Potentially-sensitive data are made available for commercial and research purposes.



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- NO!
 - \bullet Correlated public data \rightarrow De-anonymization!

We Found Joe Biden's Secret Venmo. Here's Why That's A Privacy Nightmare For Everyone.

The peer-to-peer payments app leaves everyone from ordinary people to the most powerful person in the world exposed.



Ryan Mac BuzzFeed News Reporter



Katie Notopoulos BuzzFeed News Reporter



Logan McDonald BuzzFeed Staff

S. Bakirtas, E. Erkip

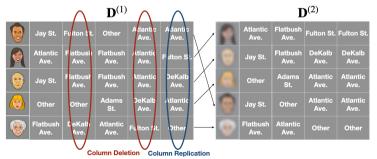


Motivation: Our Work

- Anonymized databases containing *micro-information* shared and published routinely.
- Examples: Movie preferences, financial transactions data, location data, health records.

Motivation: Our Work

- Anonymized databases containing *micro-information* shared and published routinely.
- Examples: Movie preferences, financial transactions data, location data, health records.
- This work: Time-indexed data, e.g., financial and location data
- Synchronization errors in time-indexed data: column repetitions





2 Background

- Practical Attacks
- Database Matching: Other Applications
- Theoretical Works

3 This Work

4 Main Results

5 Conclusion

Practical Database Matching Attacks

• [Narayanan and Shmatikov, 2008] De-anonymization of Netflix Prize Database using IMDB data.

• [Sweeney, 2002] De-anonymization of medical databases using voter registration data.

• [Naini et al., 2012] User identification from geolocation data.



(a) Unlabeled histograms (Day 1)

(b) Labeled histograms (Day 2)

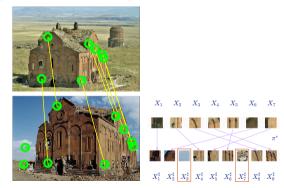
User	Location			
	Dorm.	Rest.	Lib.	
?	75%	15%	10%	
?	31%	30%	39%	
?	15%	15%	70%	
?	15%	65%	20%	

User	Location		
	Dorm.	Rest.	Lib.
John	33%	33%	34%
Jill	70%	20%	10%
Mary	15%	60%	25%
Mike	15%	20%	65%



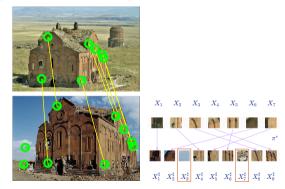
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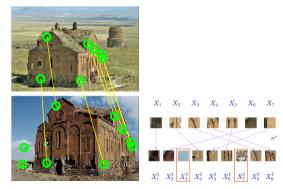


- Biological applications
 - DNA Sequencing [Blazewicz et al., 2002]

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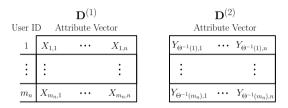
Database Matching: Other Applications

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- Biological applications
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 - Single-cell data alignment [Chen et al., 2022]

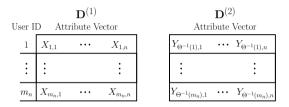
[Shirani, Garg, and Erkip, ISIT 2019]



• Databases as $m_n \times n$ random matrices: equal no. of labeled attributes (columns)

• Matching rows $\sim f_{X^{(1),n},X^{(2),n}}$

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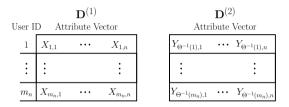
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- Successful matching: $P_e
 ightarrow 0$ as $n
 ightarrow \infty$
- Database matching ⇔ Channel decoding

• Objective: Given $(\mathbf{D}^{(1)}, \mathbf{D}^{(2)})$, find $\hat{\Theta}$ s.t.:

$$\mathsf{Pr}(\Theta(\mathit{I}) = \hat{\Theta}(\mathit{I}))
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where $I \sim U(1, m_n)$.

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- This allows us to
 - use information-theoretic tools,
 - work with arbitrary distributions.



[Bakirtas and Erkip, ISIT 2021]

- Database Matching Under Column Deletions.
 - Different numbers of attributes.
 - Attributes are unlabeled.

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• Extracting this side information from a batch of correctly-matched rows (seeds).

[Bakirtas and Erkip, Asilomar 2022]

- Matching of Markov Databases Under Random Column Repetitions.
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- Complete characterization of the matching capacity in the noiseless setting.



2 Background





5 Conclusion

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Seeded Database Matching Under Noisy Column Repetitions

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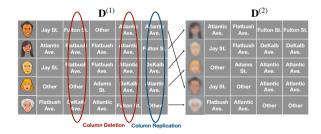
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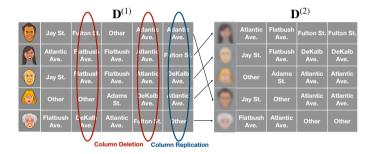
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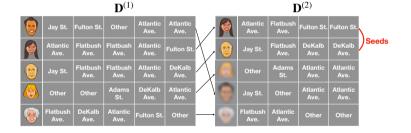
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• Column repetition pattern: random vector $S^n = \{S_1, S_2, ..., S_n\}$ with $S_j \stackrel{i.i.d.}{\sim} p_S$. • $supp(p_S) = \{0, ..., s_{max}\}$



This Work



System Model: Continued

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13 / 27

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• Goal: Given p_X , $p_{Y|X}$, p_S , d, characterize matching capacity C(d).

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- S Can we extract the repetition pattern from seeds?
- If yes, how many seeds are sufficient?

Introduction

2 Background



Main Results

- Matching Scheme
- Matching Capacity

5 Conclusion



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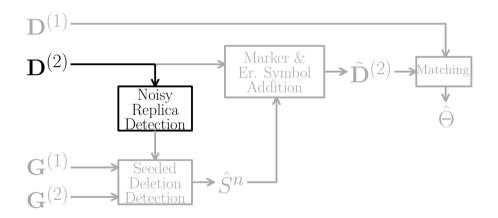


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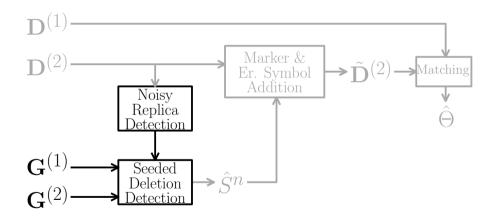


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 - **(5)** Replace the deleted columns with erasure symbols in $D^{(2)}$.
 - **O** Perform a typicality-based rowwise matching.
- We will use the *Hamming distances between the consecutive columns of* **D**⁽²⁾ as the permutation-invariant feature.

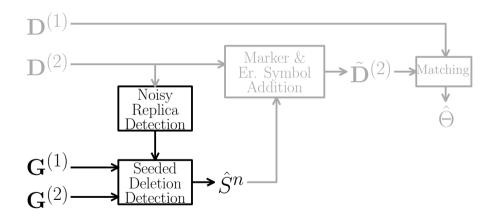




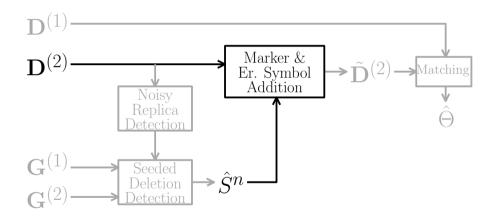




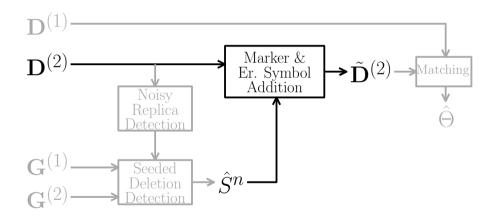




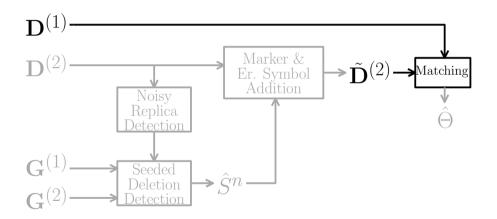




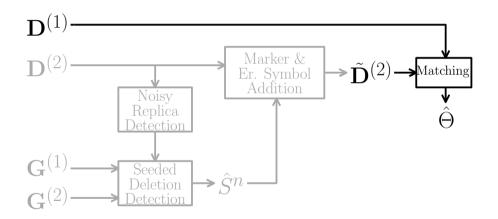














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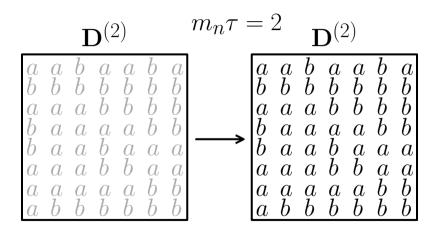


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- **③** Declare $C_j^{m_n}$ and $C_{j+1}^{m_n}$ to be
 - noisy replicas, if $d_H(C_i^{m_n}, C_{i+1}^{m_n}) < m_n \tau$.
 - independent, if $d_H(C_j^{\check{m}_n}, C_{j+1}^{\check{m}_n}) \ge m_n \tau$.

Matching Scheme



Noisy Replica Detection: Example



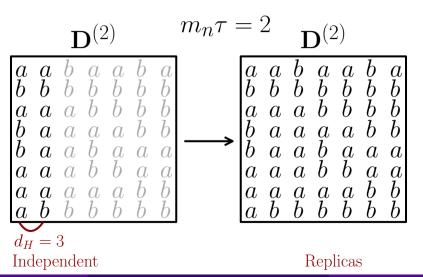
Replicas

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Matching Scheme



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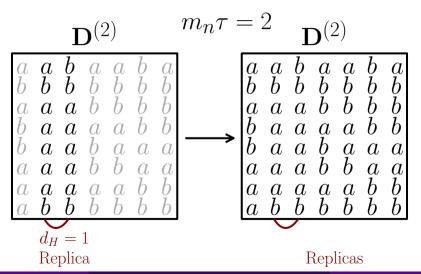


Seeded Database Matching Under Noisy Column Repetitions

Matching Scheme



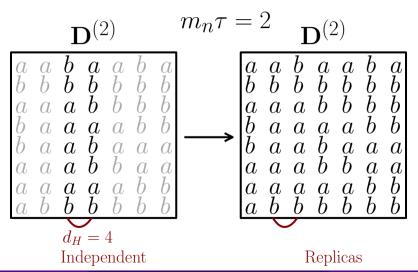
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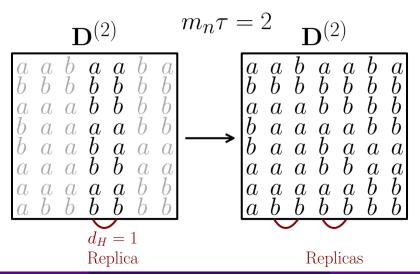
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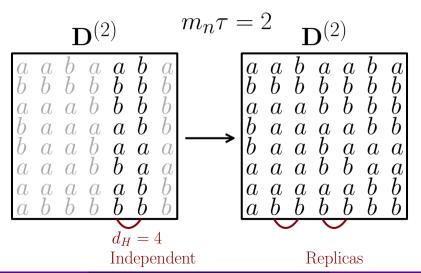


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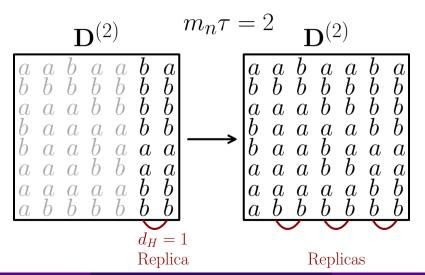
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Noisy Replica Detection

Lemma

Let E_j denote the event that the aforementioned Hamming distance based algorithm fails to infer the correct relationship between the columns $C_j^{m_n}$ and $C_{j+1}^{m_n}$ of $\mathbf{D}^{(2)}$, $j = 1, \ldots, K - 1$. Then

$$\mathsf{Pr}(igcup_{j=1}^{\mathcal{K}-1} E_j) o \mathsf{0} ext{ as } n o \infty$$



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- No seeds required for noisy replica detection!
- m_n being exponential in n is enough.



• Let $(X_1, Y_1), (X_2, Y_2) \sim p_{X,Y}$.



- Let $(X_1, Y_1), (X_2, Y_2) \sim p_{X,Y}$.
- Define

$$p_0 \triangleq \Pr(Y_1 \neq Y_2 | X_1 \perp X_2)$$
$$p_1 \triangleq \Pr(Y_1 \neq Y_2 | X_1 = X_2)$$



• Let $(X_1, Y_1), (X_2, Y_2) \sim p_{X Y}$.

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- $d_H(C_i^{m_n}, C_{i+1}^{m_n})$ follows
 - Binom (m_n, p_1) if $C_i^{m_n}$ and $C_{i+1}^{m_n}$ are noisy replicas.
 - Binom (m_n, p_0) if $C_i^{m_n}$ and $C_{i+1}^{m_n}$ are independent.



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 - Binom (m_n, p_0) if $C_i^{m_n}$ and $C_{i+1}^{m_n}$ are independent.
- Show $p_0 > p_1$ for any $p_X y \neq p_X p_Y$.



• Let (X_1, Y_1) , $(X_2, Y_2) \sim p_{X,Y}$.

$$p_0 \triangleq \Pr(Y_1 \neq Y_2 | X_1 \bot X_2)$$
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- $d_H(C_j^{m_n}, C_{j+1}^{m_n})$ follows
 - Binom (m_n, p_1) if $C_i^{m_n}$ and $C_{i+1}^{m_n}$ are noisy replicas.
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- $\Theta(n)$ summands, each decaying exponentially with m_n .





Seeded Deletion Detection Algorithm

- **1** Perform noisy replica detection on $\mathbf{D}^{(2)}$.
- 2 Discard all-but-one of the replicas from $\mathbf{G}^{(2)}$ to obtain $\tilde{\mathbf{G}}^{(2)}$.
- \bullet If necessary, apply a mapping Φ to the entries of $\tilde{\mathbf{G}}^{(2)}$ to obtain $\tilde{\mathbf{G}}^{(2)}_{\Phi}$ • Φ satisfies

$$\Pr(\Phi(Y_1) \neq X_2) > \Pr(\Phi(Y_1) \neq X_1)$$

- **O** Perform an exhaustive search over all potential deletion patterns on $G^{(1)}$.
- So For each deletion pattern *I*, compute the total Hamming distance $d_H(\tilde{\mathbf{G}}_{I}^{(1)}, \tilde{\mathbf{G}}_{\pi}^{(2)})$ between $\tilde{\mathbf{G}}_{L}^{(1)}$ and $\tilde{\mathbf{G}}_{\Phi}^{(2)}$.
- **Output** the deletion pattern $\hat{l}_{del}(\Phi)$, minimizing total Hamming distance between $\tilde{\mathbf{G}}_{\iota}^{(1)}$ and $\tilde{\mathbf{G}}_{\Phi}^{(2)}$

$$\hat{\mathit{l}}_{\mathsf{del}}(\Phi) = \mathop{\arg\min}_{\textit{I}\subseteq[n]} \mathit{d}_{\textit{H}}(\tilde{\mathbf{G}}_{\textit{I}}^{(1)}, \tilde{\mathbf{G}}_{\Phi}^{(2)})$$



Seeded Deletion Detection

Lemma

Let I_{del} be the underlying deletion pattern. Then there exists a bijective mapping Φ depending on $p_{X,Y}$ and for seed size $\Lambda_n \geq cnH_b(\delta)$,

$$\mathsf{Pr}\left(\widehat{\mathit{l}}_{\mathsf{del}}(\Phi) = \mathit{l}_{\mathsf{del}}
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- *i.e.*, a seed size logarithmic with the row size m_n is sufficient!



Detection:

• Union bound over all deletion patterns

$$\Pr\left(\hat{l}_{\mathsf{del}}(\Phi) \neq l_{\mathsf{del}}\right) \leq \sum_{I \subseteq [n], |I| = \hat{K}} \Pr(d_{H}(\tilde{\mathbf{G}}_{I}^{(1)}, \tilde{\mathbf{G}}_{\Phi}^{(2)}) \leq d_{H}(\tilde{\mathbf{G}}_{I_{\mathsf{del}}}^{(1)}, \tilde{\mathbf{G}}_{\Phi}^{(2)}))$$



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• Observe

$$\begin{aligned} & d_{H}(\tilde{\mathbf{G}}_{I}^{(1)}, \tilde{\mathbf{G}}_{\Phi}^{(2)}) - d_{H}(\tilde{\mathbf{G}}_{I_{\text{del}}}^{(1)}, \tilde{\mathbf{G}}_{\Phi}^{(2)}) = M - N \\ & M \sim \text{Binom}(\Lambda_{n}(\hat{K} - f(I, I_{\text{del}})), q_{0}(\Phi)) \\ & N \sim \text{Binom}(\Lambda_{n}(\hat{K} - f(I, I_{\text{del}})), q_{1}(\Phi)) \end{aligned}$$



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• $f(I, I_{del})$: Overlap between the retention (non-deletion) patterns output by I and I_{del} .

- Apply Hoeffding's inequality to the summands.
- Sum over $f(I, I_{del})$ instead of I.

 Y^{K} : a row of $\mathbf{D}^{(2)}$.

$$\begin{split} \tilde{Y} &= [Y_1, Y_2] * |Y_3, Y_4, Y_5|Y_6| * | \dots] \\ & & \uparrow \\ & & & \\ \hline & & \\$$

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 \tilde{Y} : the corresponding row of $\tilde{\mathbf{D}}^{(2)}$.

 V^K

S. Bakirtas, E. Erkip

ITW 2022

Main Result

Theorem: Main Result

Given a database distribution p_X , a column repetition distribution p_S and a noise distribution $p_{Y|X}$, for any seed order $d \ge 1$, the matching capacity is

$$C(d) = I(X; Y^S, S)$$

where $S \sim p_S$ and $Y^S = Y_1, \ldots, Y_S$ such that

$$\Pr(Y^{S} = y_{1}, \dots, y_{S} | X = x) = \prod_{i=1}^{S} p_{Y|X}(y_{i} | x)$$

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- Deleted columns do not offer any information.
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 - Replication acts as a repetition code
 - With (randomly) varying length.
- We have a complete characterization of the matching capacity.



2 Background









Conclusion

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 - Extension to more general database distributions.
 - Database matching when the repetition pattern is not constant across rows.

Thank you! Q&A?

Seeded Database Matching Under Noisy Column Repetitions

Serhat Bakirtas, Elza Erkip

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• This is not true in general!

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- \bullet After applying $\Phi,$ we can use the aforementioned algorithm.

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• Thus, as long as $p_{Y|X} \neq p_Y$,

 $\exists \Phi \, q_0(\Phi) > q_1(\Phi)$